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SEQUENCE LISTING

<110> The Horticulture and Food Research Institute of NZ

<120> Seedless Fruit Production

<130> 26329 MRB

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<141>

<150> NZ337688

<151> 1999-09-07

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 868

<212> DNA

<213> Malus domestica

<220>

<221> CDS

<222> (1)..(648)

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agg cag gtg acc tac tcc aag agg aat ggg att atc aag aag gca	96		
Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Ile Ile Lys Lys Ala			
20	25	30	

aag gag atc act gtt cta tgt gat gct aaa gta tct ctt atc att tat	144		
Lys Glu Ile Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Ile Tyr			
35	40	45	

tct agc tct ggg aag atg gtt gaa tac tgc agc cct tca act acg ctg	192		
Ser Ser Ser Gly Lys Met Val Glu Tyr Cys Ser Pro Ser Thr Thr Leu			
50	55	60	

aca gaa atc ttg gac aaa tac cat gga caa tct ggg aag aag ttg tgg	240		
Thr Glu Ile Leu Asp Lys Tyr His Gly Gln Ser Gly Lys Lys Leu Trp			
65	70	75	80

gat gct aag cat gag aac ctc agc aat gaa gtg gat aga gtc aag aaa		288
Asp Ala Lys His Glu Asn Leu Ser Asn Glu Val Asp Arg Val Lys Lys		
85	90	95
gac aat gac agc atg caa gta gag ctc agg cat ctg aag gga gag gat		336
Asp Asn Asp Ser Met Gln Val Glu Leu Arg His Leu Lys Gly Glu Asp		
100	105	110
atc aca tca ttg aac cat gta gag ctg atg gcc tta gag gaa gca ctt		384
Ile Thr Ser Leu Asn His Val Glu Leu Met Ala Leu Glu Glu Ala Leu		
115	120	125
gaa aat ggc ctt aca agt atc cgg gac aag cag tcc aag ttc gtc gac		432
Glu Asn Gly Leu Thr Ser Ile Arg Asp Lys Gln Ser Lys Phe Val Asp		
130	135	140
atg atg aga gac aat gga aag gca ctg gaa gat gag aat aag cgc ctc		480
Met Met Arg Asp Asn Gly Lys Ala Leu Glu Asp Glu Asn Lys Arg Leu		
145	150	155
160		
act tat gag ctg caa aaa caa cag gag atg aaa ata aaa gag aat gtg		528
Thr Tyr Glu Leu Gln Lys Gln Glu Met Lys Ile Lys Glu Asn Val		
165	170	175
aga aac atg gaa aat ggg tat cat cag agg cag ctg ggg aac tac aac		576
Arg Asn Met Glu Asn Gly Tyr His Gln Arg Gln Leu Gly Asn Tyr Asn		
180	185	190
aac aac cag cag cag ata cct ttt gcc ttc cgc gtg cag cct att cag		624
Asn Asn Gln Gln Ile Pro Phe Ala Phe Arg Val Gln Pro Ile Gln		
195	200	205
cca aat ctc cag gag aga atc taa tttagatatat cttgcatttg catgctcttt		678
Pro Asn Leu Gln Glu Arg Ile		
210	215	
ctaactagtt atattatctc tccacctctc tctctctttt catctgtcaa ggagttctta		738
agtttatgtc agatttccaa tggtttgtaa tggaaattagc ttctgttatga ggctttgttg		798
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<212> PRT

<213> Malus domestica

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Arg	Gln	Val	Thr	Tyr	Ser	Lys	Arg	Arg	Asn	Gly	Ile	Ile	Lys	Lys	Ala
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Lys	Glu	Ile	Thr	Val	Leu	Cys	Asp	Ala	Lys	Val	Ser	Leu	Ile	Ile	Tyr
			35				40					45			
Ser	Ser	Ser	Gly	Lys	Met	Val	Glu	Tyr	Cys	Ser	Pro	Ser	Thr	Thr	Leu
			50			55					60				
Thr	Glu	Ile	Leu	Asp	Lys	Tyr	His	Gly	Gln	Ser	Gly	Lys	Lys	Leu	Trp
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Asp	Ala	Lys	His	Glu	Asn	Leu	Ser	Asn	Glu	Val	Asp	Arg	Val	Lys	Lys
			85				90					95			
Asp	Asn	Asp	Ser	Met	Gln	Val	Glu	Leu	Arg	His	Leu	Lys	Gly	Glu	Asp
				100			105					110			
Ile	Thr	Ser	Leu	Asn	His	Val	Glu	Leu	Met	Ala	Leu	Glu	Glu	Ala	Leu
			115				120				125				
Glu	Asn	Gly	Leu	Thr	Ser	Ile	Arg	Asp	Lys	Gln	Ser	Lys	Phe	Val	Asp
			130			135				140					
Met	Met	Arg	Asp	Asn	Gly	Lys	Ala	Leu	Glu	Asp	Glu	Asn	Lys	Arg	Leu
	145				150				155				160		
Thr	Tyr	Glu	Leu	Gln	Lys	Gln	Gln	Glu	Met	Lys	Ile	Lys	Glu	Asn	Val
			165				170				175				
Arg	Asn	Met	Glu	Asn	Gly	Tyr	His	Gln	Arg	Gln	Leu	Gly	Asn	Tyr	Asn
			180				185				190				
Asn	Asn	Gln	Gln	Gln	Ile	Pro	Phe	Ala	Phe	Arg	Val	Gln	Pro	Ile	Gln
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Met	Ala	Arg	Gly	Lys	Ile	Glu	Ile	Lys	Leu	Ile	Glu	Asn	Gln	Thr	Asn	
1					5				10					15		

agg cag gtg acc tac tcc aag aga aga aat ggg atc ttc aag aag gct		96	
Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala			
20	25	30	
cag gag ctc acc gtt ctc tgt gat gcc aag gtc tcc ctc att atg ctc		144	
Gln Glu Leu Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Met Leu			
35	40	45	
tcc aac act aat aaa atg cac gag tat atc agc cct acc act acg acc		192	
Ser Asn Thr Asn Lys Met His Glu Tyr Ile Ser Pro Thr Thr Thr			
50	55	60	
aag agt atg tat gat gac tat cag aaa act atg ggg atc gat ctg tgg		240	
Lys Ser Met Tyr Asp Asp Tyr Gln Lys Thr Met Gly Ile Asp Leu Trp			
65	70	75	80
agg aca cac gag gag tcg atg aaa gac acc ttg tgg aag ttg aaa gag		288	
Arg Thr His Glu Glu Ser Met Lys Asp Thr Leu Trp Lys Leu Lys Glu			
85	90	95	
atc aac aat aag ctg agg aga gag atc agg cag agg ttg ggc cat gat		336	
Ile Asn Asn Lys Leu Arg Arg Glu Ile Arg Gln Arg Leu Gly His Asp			
100	105	110	
cta aat ggc ctg agc ttt gac gag ctg gct tct ctt gac gat gag atg		384	
Leu Asn Gly Leu Ser Phe Asp Glu Leu Ala Ser Leu Asp Asp Glu Met			
115	120	125	
cag tct tcc ttg gat gcc ata cgt caa agg aag tac cat gtg atc aaa		432	
Gln Ser Ser Leu Asp Ala Ile Arg Gln Arg Lys Tyr His Val Ile Lys			
130	135	140	
act cag acg gag acc acc aag aag aag gtt aag aac ttg gag caa aga		480	
Thr Gln Thr Glu Thr Lys Lys Val Lys Asn Leu Glu Gln Arg			
145	150	155	160
aga gga aac atg ctg cat ggc tat ttt gac cag gaa gca gcc ggc gag		528	
Arg Gly Asn Met Leu His Gly Tyr Phe Asp Gln Glu Ala Ala Gly Glu			
165	170	175	
gat cca cag tat ggt tat gag gac aat gag gga gac tac gaa tct gca		576	
Asp Pro Gln Tyr Gly Tyr Glu Asp Asn Glu Gly Asp Tyr Glu Ser Ala			
180	185	190	
ctt gca ttg tca aat ggg gcg aat aac ttg tac act ttc cac ctc cac		624	
Leu Ala Leu Ser Asn Gly Ala Asn Asn Leu Tyr Thr Phe His Leu His			
195	200	205	

cac cct aac ctg cac cac gga gga agc tcg ctc ggc tcc tcc att act	672
His Pro Asn Leu His His Gly Gly Ser Ser Leu Gly Ser Ser Ile Thr	
210	215
	220
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His Leu His Asp Leu Arg Leu Ala	
225	230
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atatgtgtgt ggtgtttaa tcaatgatag cactaaaaaa atccgcgcac ttgttgcttg	899
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Gln Glu Leu Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Met Leu			
35	40		45
Ser Asn Thr Asn Lys Met His Glu Tyr Ile Ser Pro Thr Thr Thr Thr			
50	55		60
Lys Ser Met Tyr Asp Asp Tyr Gln Lys Thr Met Gly Ile Asp Leu Trp			
65	70	75	80
Arg Thr His Glu Glu Ser Met Lys Asp Thr Leu Trp Lys Leu Lys Glu			
85	90		95
Ile Asn Asn Lys Leu Arg Arg Glu Ile Arg Gln Arg Leu Gly His Asp			
100	105		110
Leu Asn Gly Leu Ser Phe Asp Glu Leu Ala Ser Leu Asp Asp Glu Met			
115	120		125
Gln Ser Ser Leu Asp Ala Ile Arg Gln Arg Lys Tyr His Val Ile Lys			
130	135	140	
Thr Gln Thr Glu Thr Thr Lys Lys Lys Val Lys Asn Leu Glu Gln Arg			
145	150	155	160
Arg Gly Asn Met Leu His Gly Tyr Phe Asp Gln Glu Ala Ala Gly Glu			
165	170		175
Asp Pro Gln Tyr Gly Tyr Glu Asp Asn Glu Gly Asp Tyr Glu Ser Ala			

180	185	190
Leu Ala Leu Ser Asn Gly Ala Asn Asn Leu Tyr Thr Phe His Leu His		
	195	200
		205
His Pro Asn Leu His His Gly Gly Ser Ser Leu Gly Ser Ser Ile Thr		
	210	215
		220
His Leu His Asp Leu Arg Leu Ala		
	225	230

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<213> Artificial Sequence

<220>
<223> Description of Artificial

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<223> n represents a, c, g or t

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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Made in lab

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